

RAW SEQUENCE LISTING

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Application Serial Number: 10/712,785
Source: JFW
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RAW SEQUENCE LISTING

DATE: 10/25/2004

PATENT APPLICATION: US/10/712,785

TIME: 16:37:09

Input Set : A:\10498-00059.ST25.txt

Output Set: N:\CRF4\10252004\J712785.raw

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3 <110> APPLICANT: Donald, Coen M.
4     Pilger, Beatrice D.
6 <120> TITLE OF INVENTION: Method For Determining Protein Interaction Inhibitors
8 <130> FILE REFERENCE: 10498-00059
10 <140> CURRENT APPLICATION NUMBER: 10/712,785
11 <141> CURRENT FILING DATE: 2003-11-13
13 <150> PRIOR APPLICATION NUMBER: PCT/US02/15878
14 <151> PRIOR FILING DATE: 2002-05-20
16 <150> PRIOR APPLICATION NUMBER: US 60/291,901
17 <151> PRIOR FILING DATE: 2001-05-18
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 18
25 <212> TYPE: PRT
26 <213> ORGANISM: herpes simplex virus
28 <220> FEATURE:
29 <221> NAME/KEY: MISC_FEATURE
30 <222> LOCATION: (1)..(1)
31 <223> OTHER INFORMATION: acetylated amino acid
34 <220> FEATURE:
35 <221> NAME/KEY: MISC_FEATURE
36 <222> LOCATION: (18)..(18)
37 <223> OTHER INFORMATION: amidated amino acid
40 <400> SEQUENCE: 1
42 Ala Thr Ala Glu Glu Thr Arg Arg Met Leu His Arg Ala Phe Asp Thr
43 1           5           10           15
46 Leu Ala
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 339
52 <212> TYPE: PRT
53 <213> ORGANISM: herpes simplex virus
55 <400> SEQUENCE: 2
57 Met Thr Asp Ser Pro Gly Gly Val Ala Pro Ala Ser Pro Val Glu Asp
58 1           5           10           15
61 Ala Ser Asp Ala Ser Leu Gly Gln Pro Glu Glu Gly Ala Pro Cys Gln
62           20           25           30
65 Val Val Leu Gln Gly Ala Glu Leu Asn Gly Ile Leu Gln Ala Phe Ala
66           35           40           45
69 Pro Leu Arg Thr Ser Leu Leu Asp Ser Leu Leu Val Met Gly Asp Arg
70           50           55           60
73 Gly Ile Leu Ile His Asn Thr Ile Phe Gly Glu Gln Val Phe Leu Pro
74 65           70           75           80

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77 Leu Glu His Ser Gln Phe Ser Arg Tyr Arg Trp Arg Gly Pro Thr Ala
78                85                90                95
81 Ala Phe Leu Ser Leu Val Asp Gln Lys Arg Ser Leu Leu Ser Val Phe
82                100                105                110
85 Arg Ala Asn Gln Tyr Pro Asp Leu Arg Arg Val Glu Leu Ala Ile Thr
86                115                120                125
89 Gly Gln Ala Pro Phe Arg Thr Leu Val Gln Arg Ile Trp Thr Thr Thr
90                130                135                140
93 Ser Asp Gly Glu Ala Val Glu Leu Ala Ser Glu Thr Leu Met Lys Arg
94 145                150                155                160
97 Glu Leu Thr Ser Phe Val Val Leu Val Pro Gln Gly Thr Pro Asp Val
98                165                170                175
101 Gln Leu Arg Leu Thr Arg Pro Gln Leu Thr Lys Val Leu Asn Ala Thr
102                180                185                190
105 Gly Ala Asp Ser Ala Thr Pro Thr Thr Phe Glu Leu Gly Val Asn Gly
106                195                200                205
109 Lys Phe Ser Val Phe Thr Thr Ser Thr Cys Val Thr Phe Ala Ala Arg
110                210                215                220
113 Glu Glu Gly Val Ser Ser Ser Thr Ser Thr Gln Val Gln Ile Leu Ser
114 225                230                235                240
117 Asn Ala Leu Thr Lys Ala Gly Gln Ala Ala Ala Asn Ala Lys Thr Val
118                245                250                255
121 Tyr Gly Glu Asn Thr His Arg Thr Phe Ser Val Val Val Asp Asp Cys
122                260                265                270
125 Ser Met Arg Ala Val Leu Arg Arg Leu Gln Val Gly Gly Gly Thr Leu
126                275                280                285
129 Lys Phe Phe Leu Thr Thr Pro Val Pro Ser Leu Cys Val Thr Ala Thr
130                290                295                300
133 Gly Pro Asn Ala Val Ser Ala Val Phe Leu Leu Lys Pro Gln Lys Ile
134 305                310                315                320
137 Cys Leu Asp Trp Leu Gly His Ser Gln Gly Ser Pro Ser Ala Gly Ser
138                325                330                335
141 Ser Ala Ser
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 1235
147 <212> TYPE: PRT
148 <213> ORGANISM: herpes simplex virus
150 <400> SEQUENCE: 3
152 Met Phe Ser Gly Gly Gly Gly Pro Leu Ser Pro Gly Gly Lys Ser Ala
153 1                5                10                15
156 Ala Arg Ala Ala Ser Gly Phe Phe Ala Pro Ala Gly Pro Arg Gly Ala
157                20                25                30
160 Ser Arg Gly Pro Pro Pro Cys Leu Arg Gln Asn Phe Tyr Asn Pro Tyr
161                35                40                45
164 Leu Ala Pro Val Gly Thr Gln Gln Lys Pro Thr Gly Pro Thr Gln Arg
165                50                55                60
168 His Thr Tyr Tyr Ser Glu Cys Asp Glu Phe Arg Phe Ile Ala Pro Arg
169 65                70                75                80
172 Val Leu Asp Glu Asp Ala Pro Pro Glu Lys Arg Ala Gly Val His Asp

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173          85          90          95
176 Gly His Leu Lys Arg Ala Pro Lys Val Tyr Cys Gly Gly Asp Glu Arg
177          100          105          110
180 Asp Val Leu Arg Val Gly Ser Gly Gly Phe Trp Pro Arg Arg Ser Arg
181          115          120          125
184 Leu Trp Gly Gly Val Asp His Ala Pro Ala Gly Phe Asn Pro Thr Val
185          130          135          140
188 Thr Val Phe His Val Tyr Asp Ile Leu Glu Asn Val Glu His Ala Tyr
189 145          150          155          160
192 Gly Met Arg Ala Ala Gln Phe His Ala Arg Phe Met Asp Ala Ile Thr
193          165          170          175
196 Pro Thr Gly Thr Val Ile Thr Leu Leu Gly Leu Thr Pro Glu Gly His
197          180          185          190
200 Arg Val Ala Val His Val Tyr Gly Thr Arg Gln Tyr Phe Tyr Met Asn
201          195          200          205
204 Lys Glu Glu Val Asp Arg His Leu Gln Cys Arg Ala Pro Arg Asp Leu
205          210          215          220
208 Cys Glu Arg Met Ala Ala Ala Leu Arg Glu Ser Pro Gly Ala Ser Phe
209 225          230          235          240
212 Arg Gly Ile Ser Ala Asp His Phe Glu Ala Glu Val Val Glu Arg Thr
213          245          250          255
216 Asp Val Tyr Tyr Tyr Glu Thr Arg Pro Ala Leu Phe Tyr Arg Val Tyr
217          260          265          270
220 Val Arg Ser Gly Arg Val Leu Ser Tyr Leu Cys Asp Asn Phe Cys Pro
221          275          280          285
224 Ala Ile Lys Lys Tyr Glu Gly Gly Val Asp Ala Thr Thr Arg Phe Ile
225          290          295          300
228 Leu Asp Asn Pro Gly Phe Val Thr Phe Gly Trp Tyr Arg Leu Lys Pro
229 305          310          315          320
232 Gly Arg Asn Asn Thr Leu Ala Gln Pro Ala Ala Pro Met Ala Phe Gly
233          325          330          335
236 Thr Ser Ser Asp Val Glu Phe Asn Cys Thr Ala Asp Asn Leu Ala Ile
237          340          345          350
240 Glu Gly Gly Met Ser Asp Leu Pro Ala Tyr Lys Leu Met Cys Phe Asp
241          355          360          365
244 Ile Glu Cys Lys Ala Gly Gly Glu Asp Glu Leu Ala Phe Pro Val Ala
245          370          375          380
248 Gly His Pro Glu Asp Leu Val Ile Gln Ile Ser Cys Leu Leu Tyr Asp
249 385          390          395          400
252 Leu Ser Thr Thr Ala Leu Glu His Val Leu Leu Phe Ser Leu Gly Ser
253          405          410          415
256 Cys Asp Leu Pro Glu Ser His Leu Asn Glu Leu Ala Ala Arg Gly Leu
257          420          425          430
260 Pro Thr Pro Val Val Leu Glu Phe Asp Ser Glu Phe Glu Met Leu Leu
261          435          440          445
264 Ala Phe Met Thr Leu Val Lys Gln Tyr Gly Pro Glu Phe Val Thr Gly
265          450          455          460
268 Tyr Asn Ile Ile Asn Phe Asp Trp Pro Phe Leu Leu Ala Lys Leu Thr
269 465          470          475          480

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272 Asp Ile Tyr Lys Val Pro Leu Asp Gly Tyr Gly Arg Met Asn Gly Arg
273           485           490           495
276 Gly Val Phe Arg Val Trp Asp Ile Gly Gln Ser His Phe Gln Lys Arg
277           500           505           510
280 Ser Lys Ile Lys Val Asn Gly Met Val Asn Ile Asp Met Tyr Gly Ile
281           515           520           525
284 Ile Thr Asp Lys Ile Lys Leu Ser Ser Tyr Lys Leu Asn Ala Val Ala
285           530           535           540
288 Glu Ala Val Leu Lys Asp Lys Lys Lys Asp Leu Ser Tyr Arg Asp Ile
289 545           550           555           560
292 Pro Ala Tyr Tyr Ala Ala Gly Pro Ala Gln Arg Gly Val Ile Gly Glu
293           565           570           575
296 Tyr Cys Ile Gln Asp Ser Leu Leu Val Gly Gln Leu Phe Phe Lys Phe
297           580           585           590
300 Leu Pro His Leu Glu Leu Ser Ala Val Ala Arg Leu Ala Gly Ile Asn
301           595           600           605
304 Ile Thr Arg Thr Ile Tyr Asp Gly Gln Gln Ile Arg Val Phe Thr Cys
305           610           615           620
308 Leu Leu Arg Leu Ala Asp Gln Lys Gly Phe Ile Leu Pro Asp Thr Gln
309 625           630           635           640
312 Gly Arg Phe Arg Gly Ala Gly Gly Glu Ala Pro Lys Arg Pro Ala Ala
313           645           650           655
316 Ala Arg Glu Asp Glu Glu Arg Pro Glu Glu Glu Gly Glu Asp Glu Asp
317           660           665           670
320 Glu Arg Glu Glu Gly Gly Gly Glu Arg Glu Pro Glu Gly Ala Arg Glu
321           675           680           685
324 Thr Ala Gly Arg His Val Gly Tyr Gln Gly Ala Arg Val Leu Asp Pro
325           690           695           700
328 Thr Ser Gly Phe His Val Asn Pro Val Val Val Phe Asp Phe Ala Ser
329 705           710           715           720
332 Leu Tyr Pro Ser Ile Ile Gln Ala His Asn Leu Cys Phe Ser Thr Leu
333           725           730           735
336 Ser Leu Arg Ala Asp Ala Val Ala His Leu Glu Ala Gly Lys Asp Tyr
337           740           745           750
340 Leu Glu Ile Glu Val Gly Gly Arg Arg Leu Phe Phe Val Lys Ala His
341           755           760           765
344 Val Arg Glu Ser Leu Leu Ser Ile Leu Leu Arg Asp Trp Leu Ala Met
345           770           775           780
348 Arg Lys Gln Ile Arg Ser Arg Ile Pro Gln Ser Ser Pro Glu Glu Ala
349 785           790           795           800
352 Val Leu Leu Asp Lys Gln Gln Ala Ala Ile Lys Val Val Cys Asn Ser
353           805           810           815
356 Val Tyr Gly Phe Thr Gly Val Gln His Gly Leu Leu Pro Cys Leu His
357           820           825           830
360 Val Ala Ala Thr Val Thr Thr Ile Gly Arg Glu Met Leu Leu Ala Thr
361           835           840           845
364 Arg Glu Tyr Val His Ala Arg Trp Ala Ala Phe Glu Gln Leu Leu Ala
365           850           855           860
368 Asp Phe Pro Glu Ala Ala Asp Met Arg Ala Pro Gly Pro Tyr Ser Met

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369 865      870      875      880
372 Arg Ile Ile Tyr Gly Asp Thr Asp Ser Ile Phe Val Leu Cys Arg Gly
373      885      890      895
376 Leu Thr Ala Ala Gly Leu Thr Ala Val Gly Asp Lys Met Ala Ser His
377      900      905      910
380 Ile Ser Arg Ala Leu Phe Leu Pro Pro Ile Lys Leu Glu Cys Glu Lys
381      915      920      925
384 Thr Phe Thr Lys Leu Leu Leu Ile Ala Lys Lys Lys Tyr Ile Gly Val
385      930      935      940
388 Ile Tyr Gly Gly Lys Met Leu Ile Lys Gly Val Asp Leu Val Arg Lys
389 945      950      955      960
392 Asn Asn Cys Ala Phe Ile Asn Arg Thr Ser Arg Ala Leu Val Asp Leu
393      965      970      975
396 Leu Phe Tyr Asp Thr Val Ser Gly Ala Ala Ala Ala Leu Ala Glu
397      980      985      990
400 Arg Pro Ala Glu Glu Trp Leu Ala Arg Pro Leu Pro Glu Gly Leu Gln
401      995      1000      1005
404 Ala Phe Gly Ala Val Leu Val Asp Ala His Arg Arg Ile Thr Asp
405      1010      1015      1020
408 Pro Glu Arg Asp Ile Gln Asp Phe Val Leu Thr Ala Glu Leu Ser
409      1025      1030      1035
412 Arg His Pro Arg Ala Tyr Thr Asn Lys Arg Leu Ala His Leu Thr
413      1040      1045      1050
416 Val Tyr Tyr Lys Leu Met Ala Arg Arg Ala Gln Val Pro Ser Ile
417      1055      1060      1065
420 Lys Asp Arg Ile Pro Tyr Val Ile Val Ala Gln Thr Arg Glu Val
421      1070      1075      1080
424 Glu Glu Thr Val Ala Arg Leu Ala Ala Leu Arg Glu Leu Asp Ala
425      1085      1090      1095
428 Ala Ala Pro Gly Asp Glu Pro Ala Pro Pro Ala Ala Leu Pro Ser
429      1100      1105      1110
432 Pro Ala Lys Arg Pro Arg Glu Thr Pro Ser Pro Ala Asp Pro Pro
433      1115      1120      1125
436 Gly Gly Ala Ser Lys Pro Arg Lys Leu Leu Val Ser Glu Leu Ala
437      1130      1135      1140
440 Glu Asp Pro Ala Tyr Ala Ile Ala His Gly Val Ala Leu Asn Thr
441      1145      1150      1155
444 Asp Tyr Tyr Phe Ser His Leu Leu Gly Ala Ala Cys Val Thr Phe
445      1160      1165      1170
448 Lys Ala Leu Phe Gly Asn Asn Ala Lys Ile Thr Glu Ser Leu Leu
449      1175      1180      1185
452 Lys Arg Phe Ile Pro Glu Val Trp His Pro Pro Asp Asp Val Ala
453      1190      1195      1200
456 Ala Arg Leu Arg Thr Ala Gly Phe Gly Ala Val Gly Ala Gly Ala
457      1205      1210      1215
460 Thr Ala Glu Glu Thr Arg Arg Met Leu His Arg Ala Phe Asp Thr
461      1220      1225      1230
464 Leu Ala
465      1235

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VERIFICATION SUMMARY

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